Hindawi
BioMed Research International
Volume 2021, Article ID 5598907, 9 pages
https://doi.org/10.1155/2021/5598907

Research Article

Analysis of Biofilm-Related Genes and Antifungal Susceptibility Pattern of Vaginal *Candida albicans* and Non-*Candida albicans* Species

Faezeh Mohammadi,[1] **Nima Hemmat**,[1] **Zahra Bajalan**,[2] **and Amir Javadi**[3]

[1]*Cellular and Molecular Research Center, Research Institute for Prevention of Non-Communicable Disease, Qazvin University of Medical Sciences, Qazvin 34159-14595, Iran*
[2]*Social Determinants of Health Research Center, Qazvin University of Medical Sciences, Qazvin 34159-14595, Iran*
[3]*Department of Social Sciences, School of Medicine, Qazvin University of Medical Sciences, Qazvin 34159-14595, Iran*

Correspondence should be addressed to Faezeh Mohammadi; esf.mohamadi@gmail.com

Received 14 February 2021; Accepted 16 May 2021; Published 29 May 2021

Academic Editor: Stefania Cantore

Background. Vulvovaginal candidiasis caused by *Candida* species is a prevalent fungal infection among women. It is believed that the pathogenesis of *Candida* species is linked with the production of biofilm which is considered a virulence factor for this organism. The aim of this study was molecular identification, antifungal susceptibility, biomass quantification of biofilm, and detection of virulence markers of *Candida* species. *Methods*. We investigated the molecular identification of 70 vaginal isolates of *Candida* species, antifungal resistance to amphotericin B, fluconazole, itraconazole, and voriconazole according to CLSI M27-A3 and M27-S4, biofilm formation, and frequency analysis of biofilm-related ALS1, ALS3, and HWP1 genes. *Results*. Our findings showed that the most common yeast isolated from vaginal discharge was *C. albicans* (67%), followed by the non-*Candida albicans* species (33%). All *C. albicans* complex isolates were confirmed as *C. albicans* by HWP-PCR, and all isolates of the *C. glabrata* complex were revealed to be *C. glabrata sensu stricto* using the multiplex PCR method. FLC resistance was observed in 23.4% of *C. albicans* and 7.7% of *C. glabrata*. The resistance rate to ITC was found in 10.6% of *C. albicans*. The frequency of ALS1, ALS3, and HWP1 genes among *Candida* species was 67.1%, 80%, and 81.4%, respectively. Biofilm formation was observed in 54.3% of *Candida* species, and the highest frequency detected as a virulence factor was for the ALS3 gene (97.3%) in biofilm-forming species. *Discussion*. Our results showed the importance of molecular epidemiology studies, investigating antifungal susceptibility profiles, and understanding the role of biofilm-related virulence markers in the pathogenesis of *Candida* strains.

1. Introduction

Vulvovaginal candidiasis (VVC) is a common fungal infection in young women, and several factors such as age, diabetes, pregnancy, taking estrogen-containing birth control pills, antibacterial therapy, and the use of intrauterine devices have been identified as risk factors [1]. Vaginal candidiasis is associated with discharge, inflammation, burning, and redness. *Candida albicans* is the most important causative agent of VVC, followed by non-*Candida albicans* species [2]. The diagnosis of vulvovaginal candidiasis is often based on clinical signs and symptoms, and fluconazole is mostly used to treat *Candida* vaginitis. However, variable levels of resistance against antifungals may emerge in *Candida* species due to empirical administration or overuse of antimycotic agents [3, 4]. In recent decades, drug resistance has been increasing due to the overuse of antifungals [5, 6]. Therefore, understanding the antifungal susceptibility profiles of *Candida* species is key in guiding the selection of appropriate treatment for vulvovaginal candidiasis [6]. On the other hand, the pathogenicity of *Candida* species is increased with factors such as the ability to produce hyphae, binding and adhesion,